

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: March 26, 2003, 16:38:14 ; Search time 6.39535 Seconds (without animation)

Title: US-10-010-667A-19

Sequence: 1 REVIHPLATSHQQYFYKIPILV 22

Gapor 10.0 , Gapext 0.5

Searched: 112892 segs, 41476328 residues
Total number of hits satisfying chosen parameters:

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Query	Match	Length	DB	ID	Description
1	516	100.0	355	1	CPHES	homo sapiens	CPHES
2	438	44.2	177	1	CITG	homo sapiens	CPHES
3	47.5	40.9	320	1	MSRA	homo sapiens	CPHES
4	46	39.7	731	1	CYF	Forp	CPHES
5	46	39.7	731	1	SEYA	ARAH	CPHES
6	46	38.7	731	1	YD27	MYCUT	CPHES
7	45	38.7	1839	1	CYAA	SACXL	CPHES
8	45	38.8	2549	1	FRAP	MOUSE	CPHES
9	44.5	38.4	137	1	SPML	ERG	CPHES
10	44.5	38.4	137	1	SPML	ERG	CPHES
11	44.5	38.4	137	1	SPML	ERG	CPHES
12	44	37.9	811	1	RPB2	DROME	CPHES
13	44	37.9	928	1	RGTA	HEWB	CPHES
14	44	37.9	933	1	VGAB	HEWB	CPHES
15	43.5	37.5	326	1	YJHS	ECOLI	CPHES
16	43	37.1	337	1	DHNS	VIBCH	CPHES
17	43	37.1	372	1	EXTL	ARATH	CPHES
18	43	37.1	395	1	RYBA	ARATH	CPHES
19	42.3	36.2	216	1	MSRA	XYLEFA	CPHES
20	42	36.2	316	1	DHAS	VIEVI	CPHES
21	42	36.2	1437	1	DPO3	BASDU	CPHES
22	42	36.2	2549	1	FRAP	HUMAN	CPHES
23	42	36.2	2549	1	FRAP	RAT	CPHES
24	42	35.8	116	1	AGN3	PIG	CPHES
25	41.5	35.8	154	1	AGN3	PIG	CPHES
26	41.5	35.8	154	1	AGN3	PIG	CPHES
27	41	35.7	196	1	COAF	HEHP	CPHES
28	41	35.7	196	1	COAF	HEHP	CPHES
29	41	35.3	576	1	SBP	CARLE	CPHES
30	41	35.3	623	1	YO1	MUCPI	CPHES
31	41	35.3	635	1	XYMB	BUTFI	CPHES
32	40.5	34.9	433	1	EPED	SALDU	CPHES
33	40.5	34.9	492	1	SYNM	YEAST	CPHES

ALIGNMENTS		
RESULT 1		
STEAL HUMAN	STANDARD:	PTT: 339 AA.
ID STEAL HUMAN	056034	
DT 16-OCT-2001	Reel. 40	Created
DT 16-OCT-2001	Reel. 40	Last sequence update
DT 15-JUN-2002	Reel. 41	Last annotation update
DE	Six transmembrane epithelial antigen of prostate.	
OS	STEAP OR STEAP1.	
OS	Homo sapiens (human)	
OC	Eukaryota; Metazoa; Chordata; Carnivora; Vertebrata; Euteleostomi;	
OC	Mammalia; Primates; Hominidae; Catarrhini; Hominoidea; Homo.	
OC	NCBI_TaxId:9606;	
RN	[1] _TaxId:9606;	
RP	SEQUENCE FROM N.A.	
RK	MEDLINE=20056277; PubMed=10588738;	
RA	Hubert R.S., Vivanco I., Chen E., Rastegar S., Leong K.,	
RA	Mitchell S.C., Madrasana R., Zhou X., Kuo Y., Kallala A.S.,	
RA	"STEAP", a prostate-specific cell-surface antigen highly expressed in	
RT	human prostate tumors".	
RT	Proc. Natl. Acad. Sci. U.S.A. 96:14523-14528(1999).	
RN	[2]	
RP	SEQUENCE FROM N.A.	
RA	Abu-Tthead J., Steneking T., Langston Y., Mairin R.,	
RA	Smithed (JUN-1998) to the EMBL/Genbank/DBJ databases.	
RP	SEQUENCE FROM N.A.	
RA	TISSUE=Skin;	
RA	Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases.	
RL	SUBCELLULAR LOCATION: Integral membrane protein [Potential].	
CC	"-1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN PROSTATIC TUMORS.	
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration	
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation on	
CC	use by non-profit institutions as long as its content is in no way	
CC	modified and this statement is not removed. Usage by, and for, commercial	
CC	entities requires a license agreement (see http://www.isb-sib.ch/announce	
CC	or send an email to license@sib-sib.ch).	
DR	EMBL: AF166249; AF17479.1; -	
DR	EMBL: AC005053; AAC79150.1; ALT INT.	
DR	EMBL: AC004969; AAD15620.1; ALT INT.	
DR	EMBL: BC011802; AAH11802.1; -	
DR	Genev, HNCIC11378; STAP.	
DR	MIM: 604345; -	
FT	TRANSNMEN 71 amino acids	
FT	TRANSNMEN 119 139 POTENTIAL.	
FT	TRANSNMEN 164 184 POTENTIAL.	
FT	TRANSNMEN 218 238 POTENTIAL.	
FT	TRANSNMEN 258 278 POTENTIAL.	
FT	TRANSNMEN 291 311 POTENTIAL.	
SO	SEQUENCE 339 AA; 35443M1100870387 CRC64;	

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Query Match      49.3%   Score 52.5; DB 1; Length 465;  
Best Local Similarity 50.0%;  
Pred. No. 0.66;  
Matches    10; Conservative     4; Mismatches       5; Indels        1; Gaps         1  
  
QY          1 REVVPLPILTSHOQFFXKPI 20  
           ::-|||::|:-||:  
83 KEIRPLETGEHAFIV-LPI 101
```

	STANDARD:	PRT,	177 AA.
MSHA_HAINT_3			
AC	OSOROGO:		
DT	15-JUN-2002 (Rel. 41, Created)		
DT	15-JUN-2002 (Rel. 41, Last annotation update)		
DT	15-JUN-2002 (Rel. 41, Last sequence update)		
DE	Proteinase K (EC 3.4.21.6) (Proteinase K-like endopeptidase)		
GN	MSRA OR UNG180G		
OS	Haloaloeccium sp. (strain NRC-1).		
OC	Archaea; Euryarchaeota; Halobacteriota;		
NC	Halobacteriales;		

RX SEQUENCE FROM N. A.
 RX MEDLINE-70504483, Pubmed-1016950.
 RA Ng W. V., Kennedy S. P., Mahairs G. G., Bergquist B., Pan M.
 RA Shulka H. D., Lasby S. P., Baliga N. S., Thorsen V., Storgren J.
 RA Swartzell S., Weir D., Hall J., Dahl T. A., Welti R., Goo Y. A.
 RA Swatthauer B., Keller K. C., Cruz R., Dawson M. J., Hough D. W., La H.
 RA Waddock D. G., Jablonka S. B., Leebach P. M., Angelichiusi L., La H.
 RA Wainwright M. G., Tschopp R. E., Knecht M. P., Jung K. -H.
 RA Alam M. W., Freitas T. Hon S., Daniels C. J., Dennis P. P., Omar A. D.
 RA Eberhard H., Lowe T. W., Liang P., Riley W., Hood L., DasSarma S.
 RT "Genome sequence of *Halobacterium* species *Nod-1*".
 RL Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
 CC -1- FUNCTION: Has an important function as a repair enzyme for
 proteins that have been inactivated by oxidation. Catalyzes the
 reversible oxidation-reduction of methionine sulfoxide in proteins

CC -I- CATALYTIC ACTIVITY: Protein L-methionine + oxidized thiorodoxin =
CC protein L-methionine S-oxide + reduced thiorodoxin.
CC -I- SIMILARITY: BELONGS TO THE NSAID MET SULFOXIDE REDUCTASE FAMILY.
CC THIS ENZYME-PROTEIN IS NOT KNOWN TO BE PRODUCED THROUGH A COLLABORATION
CC BETWEEN THE Swiss Institute of Bioinformatics and the EMBL consortium.
CC Both the Swiss Institute of Bioinformatics and the EMBL consortium
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announcement>
CC or send an email to license@isb-sib.ch).

DR EMBL; AE005045; AAG19555.1; -.
DR HSRF; P54135; TEAA.
DR EMBL; AF000059; A00059; PMSR.
DR Pfam; PF001425; PMSR; 1.
DR ProDom; PD003489; PMSR; 1.
DR TrEMBL; TIGR00401; msrA; 1.
DR TrEMBL; TIGR00401; msrA; 1.
DR DDBJ/EMBL/GenBank; Complete proteome
FASTA file for *S. solfataricus* SM1149.
SO SEQUENCE 177 Aa; 1920 Mw; 337FDL2ELFDDBC RC6G4;

```

Best Local Similarity: 50.0%; Pred. No. 0.81; Indels 0; Gaps
Matches 9; Conservative 1; Mismatches 8;
Oy 2 RUTIRLASHOQYFKXP 19
| | | | |
Db 135 ERYEPAKEMQNYFEKCP 152

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SEQ 20

GenCore version 5.1.4 ps_4578
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OM protein - protein search, using sw model

Run on: March 26, 2003, 16:38:14 / Search time 9.88372 seconds
(without alignment)

142,679 Million cell updates/sec

Title: US-10-010-667a-20

Sequence: 1 RSRYRYKLWVYQVQVQKEDAVIHVWMEI 34

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing filter: 45 summaries

Database: SwissProt 40.*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	192	100.0	339	1	STRA_HUMAN
2	58.5	30.5	1418	1	CELI1_HUMAN
3	54	28.2	610	1	Y4B1_RHNS
4	52	27.1	79	1	Y0KC_BACSU
5	52	27.1	1813	1	Y013_CABEL
6	52	26.6	495	1	GLPK_SYVY3
7	51	26.6	1017	1	ACAD_SYVY3
8	50	26.0	784	1	ALP4_SCHPO
9	50	26.0	513	1	SYV1_HUMAN
10	49.5	25.8	95	1	Y04D_BACON
11	49.5	25.8	274	1	DADP_BUCAI
12	49.5	25.8	95	1	Y04D_BACON
13	49.5	25.8	274	1	DADP_BUCAI
14	49.5	25.8	350	1	Y073_MEUVA
15	49.5	25.8	940	1	SYV1_GILPN
16	49	25.5	512	1	YANA_RHNS
17	49	25.5	837	1	NK2C_HUMAN
18	49	25.5	1324	1	SVY1_BOVTE
19	49	25.5	1324	1	SVY1_BOVTE
20	49	25.5	1324	1	SVY1_BOVTE
21	48.5	25.3	339	1	Y012_CABEL
22	48.5	25.3	339	1	Y012_CABEL
23	48.5	25.3	339	1	Y012_CABEL
24	48	25.0	864	1	ACAD_MUCCA
25	48	25.0	864	1	ACAD_MUCCA
26	48	25.0	864	1	ACAD_MUCCA
27	47.5	24.7	794	1	DHG_ECOLI
28	47.5	24.7	808	1	DHG_ECOLI
29	47.5	24.7	808	1	DHG_ECOLI
30	47	24.5	244	1	YVTA_HAIJO
31	47	24.5	244	1	YVTA_HAIJO
32	47	24.5	244	1	YVTA_HAIJO
33	47	24.5	244	1	YVTA_HAIJO
34	47	24.5	244	1	YVTA_HAIJO
35	47	24.5	244	1	YVTA_HAIJO
36	47	24.5	244	1	YVTA_HAIJO
37	47	24.5	244	1	YVTA_HAIJO
38	47	24.5	244	1	YVTA_HAIJO
39	47	24.5	244	1	YVTA_HAIJO
40	47	24.5	244	1	YVTA_HAIJO
41	47	24.5	244	1	YVTA_HAIJO
42	47	24.5	244	1	YVTA_HAIJO
43	47	24.5	244	1	YVTA_HAIJO
44	47	24.5	244	1	YVTA_HAIJO
45	47	24.5	244	1	YVTA_HAIJO
46	47	24.5	244	1	YVTA_HAIJO
47	47	24.5	244	1	YVTA_HAIJO
48	47	24.5	244	1	YVTA_HAIJO
49	47	24.5	244	1	YVTA_HAIJO
50	47	24.5	244	1	YVTA_HAIJO

Result ID	Score	Match	Length	DB ID	Description
1	192	100.0	339	1	STRA_HUMAN
2	58.5	30.5	1418	1	CELI1_HUMAN
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5	52	27.1	1813	1	Y013_CABEL
6	52	26.6	495	1	GLPK_SYVY3
7	51	26.6	1017	1	ACAD_SYVY3
8	50	26.0	784	1	ALP4_SCHPO
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19	49	25.5	1324	1	SVY1_BOVTE
20	49	25.5	1324	1	SVY1_BOVTE
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22	48.5	25.3	339	1	Y012_CABEL
23	48.5	25.3	339	1	Y012_CABEL
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25	48	25.0	864	1	ACAD_MUCCA
26	48	25.0	864	1	ACAD_MUCCA
27	47.5	24.7	794	1	DHG_ECOLI
28	47.5	24.7	808	1	DHG_ECOLI
29	47.5	24.7	808	1	DHG_ECOLI
30	47	24.5	244	1	YVTA_HAIJO
31	47	24.5	244	1	YVTA_HAIJO
32	47	24.5	244	1	YVTA_HAIJO
33	47	24.5	244	1	YVTA_HAIJO
34	47	24.5	244	1	YVTA_HAIJO
35	47	24.5	244	1	YVTA_HAIJO
36	47	24.5	244	1	YVTA_HAIJO
37	47	24.5	244	1	YVTA_HAIJO
38	47	24.5	244	1	YVTA_HAIJO
39	47	24.5	244	1	YVTA_HAIJO
40	47	24.5	244	1	YVTA_HAIJO
41	47	24.5	244	1	YVTA_HAIJO
42	47	24.5	244	1	YVTA_HAIJO
43	47	24.5	244	1	YVTA_HAIJO
44	47	24.5	244	1	YVTA_HAIJO
45	47	24.5	244	1	YVTA_HAIJO
46	47	24.5	244	1	YVTA_HAIJO
47	47	24.5	244	1	YVTA_HAIJO
48	47	24.5	244	1	YVTA_HAIJO
49	47	24.5	244	1	YVTA_HAIJO
50	47	24.5	244	1	YVTA_HAIJO

Query Match 100.0%; Score 192; DB 1; Length 139;
Best Local Similarity 100.0%; Pctd. No. 9, 4e-19;

Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 RSRYRYKLNNAYVOOVONKEDNATHEHDVWMEI 34

DB 185 RSRYRYKLNNAYVOOVONKEDNATHEHDVWMEI 218

RESULT 2
CELL_CYCLEL STANDARD; PRT; 1418 AA.

AD P3461

DT 01-FEB-1994 (Rel. 28, Created)

DT 01-FEB-1994 (Rel. 28, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Ccd-11 protein.

GR Ccd-11 OR ZK512.3.

OC Genothabditis elegans; Chromodorea, Rhabdellidae; Rhabdellidae;

OC Rhabdellidae; Rhabdellidae; Genothabditis.

OC NCBI_Taxid=6239;

RA SEQUENCE FROM N.A.

RA STRAIN=Strictol N2;

RA MEDLINE=94150718; PubMed=7969398;

RA MEDLINE=94150718; PubMed=7969398;

RA MEDLINE=94150718; PubMed=7969398;

RA MEDLINE=94150718; PubMed=7969398;

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RA MEDLINE=94150718; PubMed=7969398;

RA MEDLINE=94150718; PubMed=7969398;

RA MEDLINE=94150718; PubMed=7969398;

RA MEDLINE=94150718; PubMed=7969398;

GN GAB.
OC Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.

OC NCBI_Taxid=1423;

1 RSRYRYKLNNAYVOOVONKEDNATHEHDVWMEI 34

DB 185 RSRYRYKLNNAYVOOVONKEDNATHEHDVWMEI 218

RESULT 2
CELL_CYCLEL STANDARD; PRT; 1418 AA.

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GR Ccd-11 OR ZK512.3.

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OC Rhabdellidae; Rhabdellidae; Genothabditis.

OC NCBI_Taxid=6239;

RA SEQUENCE FROM N.A.

RA STRAIN=Strictol N2;

RA MEDLINE=94150718; PubMed=7969398;

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RA MEDLINE=94150718; PubMed=7969398;

